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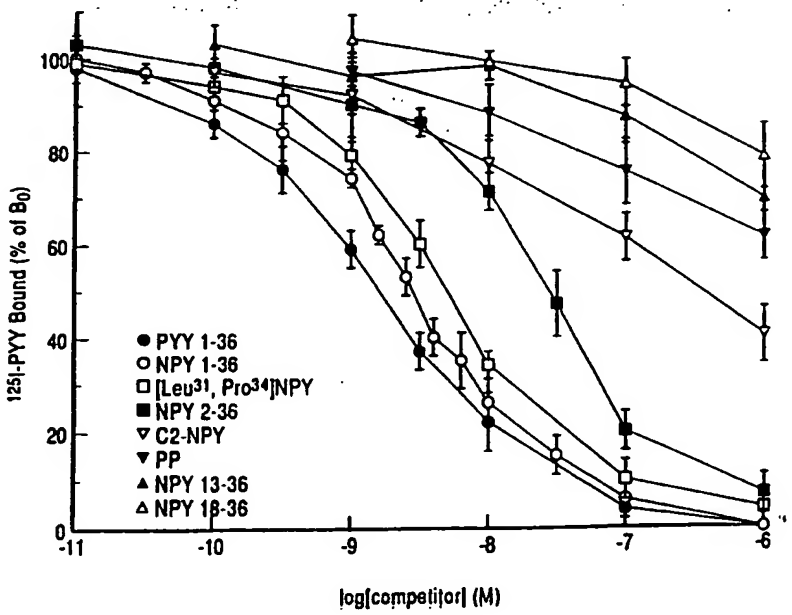

(57) Abstract

The present invention is directed to the cloning, identification and uses of the human Y-1 type neuropeptide Y/peptide YY receptor. The isolated DNA clone is expressed in COS1 cells for ligand binding competition assay. Also described is a new principle for the development of an inhibitor of the contractile responses of neuropeptide Y in human blood vessels by the use of an antisense oligodeoxynucleotide complementary to the human Y-Y1 receptor mRNA.

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HUMAN NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR OF THE Y1-TYPE AND ANTISENSE OLIGONUCLEOTIDES THERETO WHICH INHIBIT VASOCONSTRICTION

Partial funding of the research leading to the invention described herein was provided by the National Institute of Drug Abuse and the National Heart and Lung Institute. Accordingly the federal government has certain rights to this invention under 35 U.S.C.§ 200 et seq.

Under United States patent practise, this application for Letters Patent is a Continuation-in-Part application of my earlier United States Patent Application 891,453, filed May 29th 1992.

Neuropeptide Y (NPY) and peptide YY (PYY) are structurally related peptides that primarily function as neurotransmitter and gastrointestinal hormone, respectively. Previous functional and binding data have indicated the existence of at least three distinct receptor types, Y1, Y2, and Y3, for NPY and/or PYY in mammals. We describe here a human Y1 cDNA clone, hY1-5, isolated from a fetal brain library. The human Y-1 receptor consists of 384 amino acids and has seven putative transmembrane (TM) domains like other members of the G-protein-coupled superfamily of receptors. In the region spanning the TM domains, the Y-1 receptor displays 29% sequence identity to human tachykinin receptors, but it only shows 21% and 23% homology with proposed bovine (LCR1) and Drosophila (PR4) NPY-receptor clones, respectively. Northern blot analysis of a human neuroblastoma cell line, SK-N-MC, previously used by many investigators as a model system for studies on the Y-1 receptor, revealed a single 3.5 kb mRNA species. Reverse transcriptase analysis (RT-PCR) indicated expression also in human cultured vascular smooth muscle cells, supporting the view that the Y1-receptor is associated with NPY/PYY-evoked vasoconstriction. When expressed in COS1 cells, hY1-5 conferred specific ^{125}I-PYY binding sites with displacement patterns characteristic of the Y1-receptor, i.e. PYY ≥ NPY ≥ [Leu^{31}, Pro^{34}]NPY >> NPY2-36 > C2NPY > pancreatic polypeptide > NPY13-36 > NPY18-36. Moreover, in the Y1-receptor transfected COS1 cells, but not in type 1 angiotensin II receptor transfected controi cells, NPY and PYY

accelerated $^{45}Ca^{2+}$ influx and inhibited forskolin-stimulated cAMP accumulation, both phenomena being characteristic of the mammalian Y-1 receptor.

Neuropeptide Y (NPY) is a tyrosine-rich 36-amino acid peptide with a carboxyterminal amide which displays a remarkable degree of structural conservation in evolution. It is one of the most abundant and widely distributed neuropeptides within the central nervous system and belongs to a peptide family that also includes peptide YY (PYY) and pancreatic polypeptide (PP). Mammalian NPY and PYY show 70% sequence identity while PP is 50% homologous to NPY and PYY. NPY is widely distributed in the brain, notably in "limbic" regions, and the peripheral nervous system, and is often co-localized with norepinephrine, e.g. in sympathetic perivascular nerve fibers,supplying the cardiovascular system [see Trends in Pharmac. Sci. 8:231 (1987)]. In the brain many effects, including stimulation of appetite, anixiolysis/sedation and modulation of pituitary hormone release, have been attributed to NPY/PYY. Among the many peripheral actions of NPY, it has been suggested to be involved in a large number of neuroendocrine functions, stress responses, circadian rhythms, central autonomic functions, eating and drinking behavior, and sexual and motor behavior; most attention has been given to its vasoconstrictor effects. In addition, it is also possible that NPY is related to various neurological and psychiatric illnesses such as Huntington's Chorea, Alzheimer's disease, and major depressive illness. However, in the absence of specific receptor antagonists, functional studies and receptor characterizations have been difficult to perform.

Based on functional and binding data obtained from studies of various organs and cell types, it has previously been suggested that NPY/PYY receptors are heterogeneous [see Ann. NY Acad. Sci. 611:7 (1990); Regul. Pept.12:317 (1986); and Life Sci. 50: PL7 (1992)] and the nomenclature "Y1-, Y2- and Y3-receptor type "was introduced to encompass this heterologous nature. The Y1-receptor binds NPY and PYY with similar affinity, as well as the synthetic analog [Pro^{34}]NPY and analogs thereof, but C-terminal fragments of NPY and PYY have been

shown to bind poorly. In contrast, while the Y2-receptor also binds NPY and PYY with high affinity, the C-terminal fragments, e.g. NPY13-36,as well as a centrally truncated analog C2NPY [see Ann. NY Acad Sci. 611:35 (1990)], are only slightly less potent than the intact peptides at this receptor type. More recently, data from several laboratories [see Trends Pharmacol. Sci. 12:389 (1991)] have indicated the existence of a Y3-type of receptor, whose main characteristic is that PYY shows markedly lower affinity than NPY.

In order to address the structural and functional relationships of the NPY/PYY receptors the present invention pursued the isolation of receptor DNA clones using several strategies. These strategies led to the cloning of a putative human Y1-receptor cDNA clone. This clone, hY1-5, appears to be a human homolog of a previously published rat "orphan" receptor, FC5 [see FEBS Lett. 271:81 (1990)]. The latter rat clone had appeared relevant to the present invention because its expression pattern, as studied by *in situ* hybridization,was reminiscent of that of the Y1-receptor protein, as shown by receptor autoradiography. Thus, a polymerase chain reaction (PCR) product was generated corresponding to the rat "orphan" receptor. Using this, homologous human cDNA clones were isolated.

It is, accordingly, one aspect of the present disclosure is to present functional evidence identifying one such clone as a human NPY/PYY receptor of the Y1-type.

With the successful cloning of the NPY-Y1 receptor as described herein for the first time, and on the basis of the predicted mRNA sequence, another aspect of the present invention is to describe an 18-base antisense oligodeoxynucleotide sequence that corresponds to a coding region near the human Y1-receptor amino-terminus.

Still a further aspect of the present disclosure is to describe the inhibitory effect of treatment with neuropeptide Y-Y1 receptor antisense oligodeoxynucleotide on the contractile response to NPY of human arteries and veins.

The following figures, disclosure and examples are provided to allow one to receive a more complete understanding of the present

invention. These examples are not intended nor provided to limit the scope of the present invention in any manner, and it would be improper for one to interpret them as doing so (for example although Example VI depicts only a single antisense sequence, hY1-AS, this sequence is to be considered as merely a specific example of a class of antisense sequences which have similar capabilities of affecting the NPY-evoked contractile response of blood vessels as described herein).

With reference to the accompanying figures,

Figure 1 is a side-by-side comparison of Northern and Southern hybridizations;

Figure 2 depicts ligand competition for ^{125}I-PYY binding in hY1-5 (Y1-receptor) transfected COS1 cell membranes;

Figure 3 depicts the contractile effect of NPY on human subcutaneous arteries; and

Figure 4 depicts the contractiel effect of NPY on human veins.

More specifically, as will be described in detail below, Figure 1 depicts the Northern blot of human neuroblastoma cell lines probed with a human Y1 fragment, each lane containing 15 µg of total RNA. Figure 1 also depicts the Southern blot of human genomic DNA under conditions of high stringency, with each lane containing 10 µg of genomic DNA.

With regard to Figure 2, the competition data are presented as a percentage of specific binding in the absence of competitor wherein each point is the mean ± SEM of two triplicate experiments. The concentration of ^{125}I-PYY was 0.1nM. Each tube contained membranes (crude particulate fractions) from 2X10^6 COS1 cells. Non-specific binding was defined as binding in the presence of 1µM unlabeled NPY.

With respect to Figures 3 and 4, as described above, these figures depict the contractile effect of NPY on human subcutaneous (Figure 3) arteries (diameter of 0.41 ± 0.03 mm) and (Figure 4) veins (diameter of 0.43 ± 0.03 mm) expressed as a percent of the contraction induced by 60 mM KCl. To obtain the data depicted, all vessels were incubated at 37° C for 48 hours. The symbols indicate treatment with (•) 1 µM antisense, (O) 1 µM sense, (|) 1 µM mismatch or (/) control, i.e., no

oligodeoxynucleotide. As shown, the contractile response to NPY was markedly reduced after antisense treatment. Values represent the mean ± SEM; n represents 8-10, except for the mismatch where n represents 3; * represents $p<0.05$; and ** represents $p<0.01$ between sense and antisense (paired Wilcoxon signed rank test).

EXAMPLE I

Screening of a Human Fetal Brain cDNA Library

1. Human Fetal Brain cDNA Library:

The lambda ZAPII cDNA library (Stratagene) was made from mRNA of a human female fetal (17-18 week gestation) brain, using both oligo (dT) and random-sequence primers.

2. Transfer to Nylon Membranes:

After titering the fetal brain lambda ZAP cDNA library (10^9 pfu/ml), aliquots containing 50,000 phage particles were mixed with 0.2 ml of the host bacteria (XL1), which were then infected by incubating the mixture for 20 minutes at 37°C. In total, 200,000 clones were screened. Next, 6.5 ml top agarose (0.6%, at about 50°C) were added to the aliquots and poured onto 150 mm agar plates warmed to 37°C. The plates were incubated at 37°C for about 6-8 hours or until the plaques were confluent. The plates were cooled at 4°C for 2 hours before applying nylon filters. Biotrans nylon membrane (ICN) were placed onto the surface of the top agar, and markings were made with a syringe needle containing radioactive India ink for identification and orientation purposes. The filters were submerged in denaturing solution (1.5 M NaCl and 0.5 M NaOH) for 2 min and in neutralizing solution (1.5 M NaCl, 0.5 M Tris-HCl, ph 8.0) for 5 minutes, and then rinsed in 2X SSC (0.3 M NaCl, 0.03 M sodium citrate, ph 7.0). The filters were dried on Whatman 3MM paper and DNA was fixed to the filters by either using a UV Stratalinker 1800 (Stratagene) or baking at 80°C for 2 hours in a vacuum oven.

3. Probe Preparation:

A 500-bp PCR product, corresponding to part of the coding region (547-1047) of the rat orphan receptor was used to screen the human

fetal brain cDNA library. This probe was generated using the following PCR conditions: 5 min at 95°C for 1 cycle, then 1 min at 93°C, 1 min at 45°C and 2 min at 72°C for 35 cycles, with the fetal brain cDNA library as template, and a 23-mer forward primer (TTCCAAAATGTATCACTTGCGGC, positions 547-569) and a 25-mer reverse primer (TAGTCTCGTAGTCCGTCCGTCTCGAG, positions 1023-1047). Both primers were synthesized on a Biosearch Cyclone DNA Synthesizer. The PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 1.6 mM dNTPs (US Biochemical), 50 pmol of forward and reverse primers, and 1 unit Taq DNA Polymerase in a 100 µl reaction volume.

4. Probe Labeling:

The human fetal brain probe was labeled using a random primed DNA labeling kit (Boehringer Mannheim Biochemical), following the manufacturer's instructions. Approximately 25 ng of the human fetal brain PCR product was heat denatured (10 minutes at 95°C), and the following components were added: dATP, dGTP, dTTP mixture (all 0.5 mmol/l in Tris buffer); reaction mixture (10X buffer with random hexamer primers); 50 µCi [alpha-^{32}P] dCTP, 3000 Ci/mmol; and 1 unit Klenow enzyme. This mixture was incubated for 30 minutes at 37°C, and heated at 65°C for 10 minutes to stop the reaction. The probe was then purified by Sephadex G-50 Sin Columns to remove non-incorporated deoxyribonucleotide triphosphates. The Pharmacia Oligolabelling Kit was also used to label the human fetal brain probe.

5. Hybridization Conditions:

The filters were prehybridized for 2 hours at 42°C in 25% formamide, 1 M NaCl, 10% dextran sulfate, 5X Denhardt's solution and 1% SDS. The hybridization was carried out in the same solution with the addition of the ^{32}P-labeled human fetal brain probe (300 µl volume, 200-300 cps/µl) at 42°C for 16 hours. The filters were then washed twice for 5 minutes at room temperature in 2X SSC, 0.2% SDS and twice at 42°C for 30 minutes in 2X SSC, 0.5% SDS. The nylon membranes were exposed to XAR-5 (Kodak) film at -70°C for 24-72 hours.

6. Secondary Screening:

The positive plaques were removed from the plates and placed in SM buffer ((0.1 M NaCl, 0.01 M $MgSO_4$, 50 mM Tris-HCl (pH 7.5), and 0.01% gelatin)). These plaques were diluted and titered with XL1 cells to yield about 10 plaques for the first set and 100 plaques for the second set on 100 mm agar plates. As before, the plates were incubated at 37°C overnight and transferred to nylon membranes as previously described. The same prehybridization/hybridization conditions in the initial screening were also used for the secondary screening. Positive clones were chosen for the tertiary screening, which was carried out essentially as described for the secondary screen.

After isolating single positive plaques from the human fetal brain library, 8 were chosen for further restriction enzyme and sequence analysis. The next step is to sequence these cDNA clones to determine whether any of them are homologous to the rat receptor, and if so, whether any of these candidates are full length clones, which is critical for functional expression studies of potential NPY/PYY receptor cDNAs.

EXAMPLE II

Sequencing cDNA Clones

1. In vivo Excision of pBluescript Plasmid from Lambda ZAP Vector:

Phagemids were rescued from the lambda vector and transfected into XL1 Blue bacteria according to the Stratagene protocol. The single positive plaques from the agar plates were removed and placed into a solution containing SM buffer and chloroform in Eppendorf tubes. The samples were incubated at room temperature for one hour, with occasional vortexing, after which 0.2 ml of the plaque samples were added to 0.2 ml XL1-Blue cells (OD_{600} =1.0) and 1 µl of R408 helper phage, and this was incubated at 37°C for 15 minutes. The 5 ml of 2X YT media (10 g NaCl, 10 g Yeast extract and 16 g Bacto-Tryptone/liter) were added to the samples and incubated for another 3 hrs at 37° C. Next, the samples were heated at 70° C for 20 minutes and centrifuged at 4000 x g for 5 min. The supernatant, containing the pBluescript

phagemid, was collected and 10 µl was removed, and combined with 200 µl XL1-Blue cells (OD_{600} = 1.0), which was incubated at 37° C for 15 min. Subsequently, 20 and 50 µl of these transfected cells were plated onto 100 mm LB/ampicillin plates and incubated overnight at 37° C.

2. Plasmid DNA Purification:

The Bluescript vector was purified from colonies using Promega Magic Miniprep system. The minipreps were performed according to the manufacturer's protocol. Overnight cultures were pelleted by centrifugation, and the pellets were resuspended in Cell Resuspension Solution (50 mM Tris-HCl, pH 7.5, 10 mM EDTA, 100 µl/ml RNase A). Cell lysis solution (0.2 M NaOH, 1 mM EDTA) was added to the resuspended cells, and then the cells were neutralized in a solution of 2.55 M KOAc, pH 4.8. After spinning the samples in a microcentrifuge (14,000 x g for 5 min), the supernatant was collected and the DNA purification resin (Promega) was added before application to the mini-column. The mini-colum,n containing the DNA-bound resin was rinsed with Column Wash Solution (100 mM NaCl, 10 mM Tris-HCl, pH 7.5, 2.5 mM EDTA and 50% ethanol); afterwards it was placed in a microcentrifuge tube, which was spun quickly to dry the resin. The plasmid DNA was eluted with pre-heated water (65-70°C) and respun, and the purified DNA was collected. After restriction enzyme characterization of the plasmid DNA, suitable clones were chosen for sequence analysis.

2.1 Manual Sequencing Procedure:

Prior to the sequencing reaction, the double-stranded Bluescript plasmid obtained from the miniprep procedure was alkali denatured (incubation at 37° C for 30 min. in 0.2 M NaOH, 0.2 mM EDTA), neutralized in 0.4 volume 5 M NH_4Ac and precipitated with 4 volume 100% ethanol at -70° C for 5 min., after which it was spun in a microcentrifuge and the pellet was washed with 70% ethanol. The sequencing was performed using The Sequenase Version 2.0 Sequencing kit (US Biochemical) and the sequencing reactions were carried out according to the manufacturer's instructions. Sterile water was added

to the pelleted DNA, resuspended, and the following components were also added: 5X sequencing buffer (200 mM Tris-HCl, pH 7.5, 100 mM $MgCl_2$, 250 mM NaCl), 3-4 pmol primer (T3, T7, SK, KS, M13 and M13 rev were synthesized on an ABI 394 DNA/RNA Synthesizer). The primers were annealed to the plasmid by heating at 65°C for 2 min. and then cooled at room temperature. Each of the four termination mixtures were pipetted into microtiter plate wells. The 5X labeling Mix (7.5 um each of dGTP, dCTP, dTTP) was diluted with water, and the Sequenase was diluted in the enzyme dilution buffer (10 mM Tris-HCl, pH 7.5, 5 mM DTT and 0.5 mg/ml BSA). For the labeling reaction, 0.1 M DTT, diluted labeling mix, 5 µCi [^{35}S]-dATP (Amersham, >1000 Ci/mmol) and diluted sequenase were added to the annealing mixture and incubated at room temperature for 5 min. For the termination reaction, the labeling reaction was added to each of the termination mixtures, and incubated for 5 min at 37° C. After this incubation, stop solution (95% formamide, 20 mM EDTA, 0.05% bromphenol blue and 0.05% xylene cyanol) was added to each reaction. The sequencing reactions were also carried out with the Pharmacia T7 sequencing kit using their sequencing protocol, which is similar to the procedure described above.

3. Automated Fluorescence Based Solid Phase Sequencing:

Sequencing of the HY1-5 and HY1-7 clones were performed by using the manual dideoxy chain termination reaction using T7 DNA-polymerase and ^{35}S-ATP (described above) and by using a Taq-polymerase based dideoxy chain termination reaction with dye-labeled 2',3'-dideoxynucleoside triphosphates, where the sequencing reaction is separated on an automated DNA sequencing apparatus (Applied Biosystems 373A Sequencing System) that automatically collects sequence data and makes it possible to export sequences to a databank, where further analysis of the sequence can take place. The procedure for sequencing the human Y1 receptor by using Taq-polymerase based dideoxy chain termination reactions with dye-labeled 2',3'-didoxynucleoside triphosphates follows the protocol described below. All PCR reactions were performed on thermal cyclers from Perkin-Elmer.

3.1 Insert PCR of a DNA cloned in a plasmid and binding to a solid phase:

Two oligonucleotides (primers), JS1 (5'-GCGCGGATAACAATTTCACACA-3') and JS2 (5'-GCAGCACTGACCCTTTTGGGACCG-3') were constructed. They correspond to the sequences juxtaposed to the linker of the PUC plasmid and its derivatives, making it possible to do PCR amplification of a DNA cloned in the plasmid's linker. A second set of the JS-primers, called JS1B and JS2B, were modified by coupling biotin to the primer's 5'-end. Biotin is a protein that strongly binds a 66 kDa protein called Streptavidin. A PCR-reaction where one primer is biotinylated and the other is not generates a product that can be bound to a solid phase, in our case the Dynalbeads M-280 (ny Dynal, Norway) complexes between superparamagnetic polystyrene beads chemically bound to Streptavidin. Once the biotinylated product is bound to streptavidin the product can be denatured and the non-bound DNA can be washed away, resulting in single stranded DNA bound to the magnetic beads. The standard PCR insert amplification protocol is:

Ten picomoles of each primer (either JS1-JS2b or JS1B-JS2, depending on each strand that shall be sequenced), 10-100 picograms of plasmid-DNA in a PCR reaction that contains 50 mM KCl, 10 mM Tris-HCl (pH 8.4), 1.5 mM $MgCl_2$, 0.8 mM dNTPs (Pharmacia), and 1 unit of Taq polymerase (Perkin-Elmer) in a 50 µl reaction volume.

Binding of the PCR generated product and separation of the two strands were achieved following the protocol:

1) Add 20 µl (0.2 mg) of the Dynalbeads to a magnetic Eppendorf stand. This will precipitate the beads immediately. Wash the Dynalbeads two times with a 200 µl SAMAG-solution (10 mM Tris-HCl, pH 7.0, 1 M NaCl, 0.1% Triton X-100).

2) Transfer the tubes with the beads to a non-magnetic stand. Add 20 µl of the PCR mixture with the biotinylated product and incubate on a shaker for 30 minutes at room temperature.

3) Transfer the tubes to a magnetic stand. Wash the beads once with 200 µl SAMAG.

4) Transfer the tubes with the beads to a non-magnetic stand. Denature the DNA by adding 200 µl denaturation solution (0.1 M NaOH, 1 m NaCl). Incubate 15 minutes at room temperature.

5) Transfer the tubes to a magnetic stand. Wash once with 200 µl of the denaturing solution. Wash once with 100 µl of a 5 x PCR buffer (400 mM Tris-HCl pH 8.9, 100 mM Ammonium Sulfate, 25 mM $MgCl_2$) diluted 1:5.

6) Transfer the tubes with the beads to a non-magnetic stand. Dissolve each sample in 6 µl of ddH_2O. Aliqout the dissolved beads into four tubes marked A (1 µl), C (1 µl), G (2 µl), and T (2 µl). (See below "B. Aliquoting the reagents")

3.2 Fluorescent DNA Taq sequencing:

The dye primers, M13, M13rev, T3 and T7 and Taq-sequencing kit were purchased from ABI. Sequencing reactions were performed according to the manufacturer's protocol.

A. Diluting the enzyme

Mix 0.5 µl AmpliTaq DNA polymerase (8 units/µl) with a 1.0 µl 5 x PCR buffer (400 mM Tris-HCl pH 8.9, 100 mM Ammonium Sulfate, 25 mM $MgCl_2$) and 5.5 µl H_2O.

B. Aliquoting the reagents

Aliquot the reagents into four 0.5 ml microcentrifuge tubes according to the following protocol:

Reagent	A	C	G	T
d/ddNTP Mix	1 µl	1 µl	2 µl	2 µl
Dye primer (0.4 pmol/µl)	1 µl	1 µl	2 µl	2 µl
5 x PCR buffer	1 µl	1 µl	2 µl	2 µl
DNA template	1 µl	1 µl	2 µl	2 µl
Diluted Taq	1 µl	1 µl	2 µl	2 µl
Total Volume	5 µl	5 µl	10 µl 1	10 µl

Overlay each of the four reactions with about 20 µl mineral oil.

C. Cycling the reactions

Place the tubes in a thermal cycler preheated to 95°C. For the present invention, a modified PCR cycle was used which included 1

minute at 94°C, 1 min at 55° C, and 1 min at 72° C for 25 cycles followed by a soak file at 4° C. These PCR conditions appeared to be as efficient as the conditions recommended by the manufacturer.

D. Concentrating the sample

In a separate tube mix 80 µl 95% ethanol with 1.5 µl 3 M sodium acetate (pH 5.3). Pipette the extension reaction from the bottom of each of the four tubes into the ethanol mixture. Mix thoroughly. Precipitate at room temperature for 10-15 minutes. Spin in a microcentrifuge for 30 minutes. Rinse the pellet with 70% ethanol and spin for another 5 minutes. Dry the pellet in a vacuum centrifuge for 1-3 minutes.

E. Loading the sample

Prior to loading, samples were resuspended in 6 µl of deionized formamide/50 mM EDTA (pH 8.0) in the proportions 5:1. Heat the sample at 90° C for 2 min. and load immediately on a pre-electrophoresed gel.

3.3 The ABI 373A Apparatus

The apparatus is based on a four-dye, one lane, scanned laser technology. Conventional 6% polyacrylamide gels are used ((57 g acrylamide, 3 g bis-acrylamide, 450 g urea and 100 ml 10 x TEB)/liter). The settings on the machine to perform a 14 hour long run are based on the manufacturer's recommendations: 2500 V, 40 mAMP, 30 W, 40°C.

The chromatograms obtained after a gel run on the ABI 373A (equivalent to the autoradiographs when reactive isotopes are used) were examined in detail by using Seqed™, the Macintosh compatible software from ABI, that allows editing of the collected sequence. The sequences were then exported to a VAX computer that has access to the UWGCG (University of Wisconsin Genetics Computer Group) package and many sequence banks (e.g. GenBank, EMBL, Swiss-prot.). The sequences were transferred by using the shareware Xferit 1.5 by Falkenburg.

The alignment of all the sequences obtained from manual and automated sequencing was created as a project called HCY1 by using a program package consisting of e.g. Gelstart, Gelenter, and Geloverlap. Gelassemble All computer work was done by using a Macintosh LC connected to a Localtalk net, allowing communication with the VAX

computer via the Public software Telnet MacTCP communication program (NSCA Software Development).

4. Gel Electrophoresis:

The sequencing reactions were incubated at 75° C for 2 min before they were run on 6% acrylamide gels (57 g acrylamide, 3 g bis-acrylamide, 480 g urea/liter in 1X TBE buffer). The gels were 0.4 mm thick and 30 cm x 38 cm in size. After the samples were run, the gel was dried (1 hr at 80° C) with a gel dryer, and exposed to XAR-5 film for 18-72 hrs.

Enzyme digestion of rescued plasmids revealed several overlapping sibling clones, of which suitable clones, i.e. the longest (hY1-5) and those containing overlapping coding regions, were selected for sequencing analysis. In addition, 4 specific synthetic primers (3 forward primers: CTCTTGCTTATGGA/GGCTGTGA, TATGTAGGTATTGCTGTGATTTG, TATACCACTCTTCTC/TT/CTGGTGCTG and one reverse primer, CTGGAAGTTTTTGTTCAGGAAT/CCCA were used for manual sequencing of the hY1-5 clones and its deletion constructs (Eco RV, Xho, Nsi-Sac and Nsi-Eco RV). The clone of interest (hY1-5) was then further characterized by Northern blot hybridization in order to estimate its mRNA size, and by Northern blots and RT-PCR to examine its distribution. Southern hybridizations were also performed to determine the number of copies of this gene present in the human genome.

EXAMPLE III

Northern and Southern Hybridization

1. Preparation of mRNA:

The mRNA from several neuroblastoma cell lines (SK-N-MC, IMR, SH-SY-5Y, LAN1, LAN2, LAN5, 1523, 2674) were purified by standard guanidinium isothiocyanate/oligo (dT)-cellulose methods. Briefly, cultured cells were homogenized in guanidinium thiocyanate homigenization buffer (4 M guanidinium thiocyanate, 0.1 M Tris-HCl, pH 7.5, 1% beta-mercaptoethanol, 0.5% sodium lauryl sarcosinate) and the resulting lysate was centrifuged (5000 x g, 20 min). After collecting

the supernatant, 0.1 vol 3M sodium acetate (pH 5.2) and 0.5 vol cold 100% ethanol were added and incubated on ice for 2 hrs. The nucleic acid was pelleted by centrifugation (as above), and the pellet was resuspended in a second guanidinium thiocyanate buffer (4 M guanidinium thiocyanate, 0.1 M sodium acetate, pH 7.0, 1 mM DTT, 20 mM EDTA, pH 8.0). The nucleic acid was precipitated in 0.5 vol cold 100% ethanol and incubated at -20° C for 2 hrs. The nucleic acid was pelleted as before, and precipitated twice more. The final pellet was resuspended in 20 mM EDTA (pH 8.0) and 1 volume chloroform: 1-butanol (4:1). This was recentrifuged as before and extraction with phenol/chloroform/isoamyl alcohol was repeated. To precipitate the RNA, 3 volumes of 4 M sodium acetate (pH 7.0) was added to the last aqueous phase, incubated at -20° C for 2 hrs before centrifugation, after which two more rounds of ethanol precipitation were carried out and the RNA was dissolved in water. The total RNA was heated at 65° C for 5 min before addition of loading buffer (20 mM Tris-HCl, pH 7.6, 0.5 M NaCl, 1 mM EDTA, pH 8.0, 0.1% sodium lauryl sarcosinate), which was then applied onto oligo (dT)-cellulose columns. The columns were washed with the loading buffer and the poly (A) RNA was eluted with the elution buffer (10 mM Tris-HCl, pH 7.6, 1 mM EDTA, pH 8.0, 0.05 SDS) and the collected poly(A) was precipitated in 0.1 volume 3 mM sodium acetate (pH 5.2) and 2.5 volumes cold ethanol. After incubation at -20°C, this RNA was pelleted by centrifugation (10,000 x g for 30 min) and was dissolved in water.

2. Transfer of mRNA to Nylon Membranes:

The mRNA (few µg) was run on formaldehyde-containing agarose gels and transferred to nylon filters by capillary elution and RNA was crosslinked to the nylon membranes using a UV Stratalinker 1800 (Stratagne).

3. Hybridization Conditions:

The probe, a 1.4 kb XhoI-EcoRI fragment of hY1-5, was labeled with ^{32}P as described earlier in Example I. The prehybridization conditions were carried out as described for cDNA screening, except that 2X SSC was used instead of 1 M NaCl. The filters were washed

using the previously outlined conditions (for cDNA screening), with the exception that the final two washes were done at 65° C in 0.2 X SSC and 0.1% SDS. The filters were exposed to film as described earlier.

4. Southern Hybridization:

The human leucocyte genomic DNA was prepared (by standard procedure) and digested with restriction enzymes. This DNA was then run on a 1% agarose gel and the DNA was transferred to filters as described before. The probe, hybridization and washes were also as described for the Northern hybridization.

The Northern hybridization showed that the hY1-5 fragment hybridized to a single 3.5 kb transcript in SK-N-MC, which was known to express Y1 receptors, whereas the probe failed to identify Y1 transcripts in several other neuroblastoma cell lines. The Southern hybridization results suggests that the genome contains a single Y1 receptor gene. In order to confirm that the cDNA clones were the human Y1 receptor, specific primers synthesized for sequencing the clones, were used in RT-PCR.

EXAMPLE IV

Reverse Transcription-PCR

1. RNA Preparation:

A. The mRNA was prepared from SK-N-MC cells using the Fast Track mRNA Isolation Kit (Invitrogen), following their instructions. In brief, cells were washed in PBS, pelleted by centrifugation, resuspended and lysed in lysis buffer (kit), and subsequently homogenized in a Dounce homogenizer. The lysate was passed through a 21 gauge needle several times, incubated at 45° C for 2 hrs, and added to pre-equilibrated oligo (dT) cellulose and incubated for another hour at room temperature with shaking. The oligo (dT) cellulose-bound mRNA was pelleted by centrifugation and resuspended in binding buffer (kit); this was repeated three times before the samples were loaded onto spin columns and quickly spun to remove excess buffer. Next, the oligo (dT) cellulose was resuspended in elution buffer and respun, after which the eluted mRNA was collected and precipitated in 0.15 volume 2

M sodium acetate and 2.5 volumes 100% ethanol. The RNA was pelleted and resuspended in elution buffer, and stored at -70° C until used.

B. Cytoplasmic RNA was prepared from human cultured circumflex coronary artery smooth muscle cells. As before, cells were washed in PBS, centrifuged, and resuspended in lysis buffer (50 mM Tris-HCl, pH 8.0, 100 mM NaCl, 5 mM $MgCl_2$, 0.5% NP-40; also added RNase inhibitor). After incubating on ice for 5 min, the lysate was centrifuged, and the supernatant was collected. Proteinase K (100 µg in 100 mM Tris, pH 7.5, 12.5 mM EDTA, 0.15 M NaCl, 1% SDS) was added to the supernatant, and incubated for 15 min at 37° C. The RNA was extracted with 2 sets of phenol/chloroform/isoamyl alcohol extractions and precipitated with 1 volume isopropanol. The cytoplasmic RNA was pelleted by centrifugation and redissolved in water.

2. Reverse Transcription Reaction:

The reverse transcription reaction was performed using the cDNA Cycle kit (Invitrogen). Approximately 1 µg of SK-N-MC mRNA (or 5 µg of circumflex coronary artery smooth muscle cell total RNA) was used in each reaction, which consisted of 10 mM MeHgOH, 0.1 M beta-mercaptoethanol, 0.2 µg of oligo dT primer, RNase inhibitor, 5X buffer, 1 mM dNTPs and 5 units reverse transcriptase. For the total RNA sample, the primer was first incubated at 65° C for 2 min before the addition of the other reagents. The samples were incubated at 42° C for one hour, followed by another incubation at 95° C for 3 min, after which another 5 units of reverse transcriptase was added and the cDNA synthesis was repeated. The resulting cDNA was used directly for PCR analysis.

3. Polymerase Chain Reaction:

The four primers synthesized for the sequencing reaction (Example II) were also used for the PCR reaction. The same PCR reagents were used as described in the probe preparation section (Example I; 50 pmol of forward and reverse primers), however, the cycling conditions were slightly different: 5 min at 95° C for 1 cycle, then 1 min at 93° C, 2 min at 55° C and 2 min at 72° C for 35 cycles.

The resulting PCR products were run on 1.5% agarose gels along with molecular weight markers to estimate their sizes.

EXAMPLE V

Functional Expression

The cDNA of the human NPY Y1 receptor was transfected into COS 1 cells. This was done in order to establish the functional identity of our clone. Following the transfection procedure described below, the cells were studied with respect to: (i) radioreceptor binding using ^{125}I-peptide YY (PYY); (ii) cyclic AMP accumulation by use of radioimmunoassay kit (Advanced Magnetics); and (iii) $^{45}Ca^{2}$ influx into the cells from the extracellular space. The two latter so-called second messenger responses were elicited by stimulation of the cells with NPY. In all three types of assay, cells not transfected with the Y1 receptor cDNA were used as controls to verify that these COS 1 cells do not normally possess Y1 receptors.

All steps of the transfection procedure were carried out under a sterile hood with the exception of purification and ethanol precipitation of the plasmid. Dulbecco's Modified Eagle Media (DMEM) contains 1% Penicillin-Streptomycin in all procedures unless otherwise specified.

1. COES 1 cells, passages 6 to 17, were maintained in T75 flask in DMEM supplemented with 10% fetal calf serum (GIBCO-BRL) at 37° C and 95% humidity under 5% CO_2 avoiding confluency until used.

2. The day before transfections were performed,cells were trypsinized and washed with 25 ml of DMEM containing 10% NuSerum (Collaborative Research; Catalogue #5000) to completely remove trypsin. After trituration, cells were subcultured to the density of 220,000 cells per 35 mm plate in 2 ml DMEM with 10% NuSerum. Allow approximately 20 hours for cells to attach to plates under the same culture-incubator condition described above.

3. On the day of transfection, the purified plasmid (cDNA of human NPY Y1 receptor in PCDM8 vector (Invitrogen) was precipitated with ethanol and dissolved in sterile 20 mM HEPES buffer (pH 7.4) containing 150 mM

NaCl to the final concentration of 0.1 mg/ml. Mix 2 µg plasmid with 15 µg DEAE-dextran (stock solution 50 mg/ml) in a volume less than 50 µl in a polystyrene tube. The final concentration of DEAE-dextran should be 500 µg/ml after mixed with media for transfections. Leave the mixture at room temperature until the media for the transfection is prepared (10 minutes). At this concentration of plasmid, normally no precipitation was formed, however, if any precipitate was visible, the volume of buffer was increased to 100 µl.

4. Combine 1.5 ml DMEM containing 10% NuSerum with chloroquin phosphate (stock solution 75 mM) to the final concentration of 75 µM, then add the media to the plasmid DEAE-dextran mixture, mix and lay it over cells. Typically the transfection mixtures were prepared in a batch when it was performed in a number of 35 mm plates. For example, for 50 plates of 35 mm diameter, 100 µg plasmid was mixed with 750 µl of 50 mg/ml DEAE-dextran, to which 75 ml DMEM media with 10% NuSerum and 75 µM chloroquin phosphate was added. After thorough mixing by pipetting up and down, 1.5 ml of the mixture was added to each plate.

5. After incubation at 37° C and 95% humidity under 5% CO_2 for 3.5 hours, not exceeding 4 hours, cells were shocked by incubating in 2 ml 10% DMSO (in Hank's balanced salt solution with Mg^{2+} and Ca^{2+}) for 1 minute. Cells were then washed with 3 ml DMEM containing 10% NuSerum and further incubated for 64-72 hours in 7 ml DMEM with 10% fetal calf serum under the incubator condition described above.

6. For the transfection using 145 mm plates, cells were subcultured to 2.8×10^6/plate in 15 mk DMEM with 10% NuSerum. Immediately before transfection, the media was replaced with 9 ml of fresh one containing 75 µM chloroquion phosphate. Transfection mixture for each plate contained 25 µg plasmid and 100 µl 50 mg DEAE-dextran in 1 ml DMEM with 10% NuSerum and 75 µM chloroquin phosphate. The mixture was then added to the cells by dropwise over the media and the plate was gently swirled to achieve the uniform mixing.

7. The cells grown in 145 mm plates were washed three times, harvested and suspended in 50 mM ice-cold Tris-HCl buffer (pH 7.4)

with 5 mM EDTA and 1 mM β-mercaptoethanol and then homogenized using Polytron (Brinkman; setting 6) for 10 sec. The homogenate was centrifuged at 1,000 x g for 10 min using a swinging bucket rotor. The supernatant was then subjected to ultracentrifugation at 100,000 x g for 30 min. The resulting pellet was resuspended by Polytron homogenizer in fresh binding buffer (137 mM NaCl, 5.4 mM KCL, 0.44 mM KH_2PO_4, 1.26 mM $CaCl_2$, 0.81 mM $MgSO_4$, 20 mM HEPES, 0.3% bovine serum albumin and 0.01 % bacitracin; pH 7.4) and membranes from 2 X 10^6 cells were used per assay tube in a final volume of 0.4 ml. Samples were then incubated with ^{125}I-peptide YY ((^{125}I-PYY (New England Nuclear); 2200 Ci/mmol; 22°C; 100 min)). In displacement-type experiments, 0.1 nM radioligand was used. The incubations were terminated by centrifugation (Eppendorf Microfuge) for 2 min, followed by washing of the pellets' surface by 1 ml ice-cold buffer. Pellets were counted in a Packard gamma-counter. Binding data were analyzed using LIGAND™ and KINETIC™ (Biosoft).

8. Cells grown in 35 mm dishes were used for $^{45}Ca^{2+}$ influx studies or cAmp studies:

A. $^{45}Ca^{2+}$ influx:

Prior to influx studies, transfected (60 hours earlier) and control transfected COS 1 cells were washed three times with 1.5 ml of the above described binding buffer solution fortified with 10 mM glucose. $^{45}Ca^{2+}$ influx (Amersham Corp; 3-5 μM; 6-10 μCi) was studied over 2 minutes with or without agonist. Final volumes were 1 ml and experiments were performed at room temperature with solutions kept at 37° C prior to use. The uptake was terminated by rapid aspiration of the incubation mixture. Cells were then washed four times with ice cold buffer in order to remove the residual extracellular radioactivity and lysed with 1 ml of lysis buffer (8 M urea, 3 M acetic acid, and 2% Nonidet P-40). The amount of $^{45}Ca^{2+}$ influx into the cells was estimated by counting the disintergrations per minute (DPM) of lysate aliquots in a liquid scintillation system after mixing with Formula 989 (New England Nuclear).

B. Cyclic AMP accumulation determination:

Sixty hours after transfection (35 mm wells) cells were equilibrated in the HEPES-based buffer described above for one hour. Phosphodiesterase inhibitor, methylisobutylxanthine (500 µM) was present throughout the cAMP experiments. Ten minutes after addition of 100 nM NPY, the cells were challenged with 5 µM forskolin. Fifteen minutes later, the reaction was terminated by adding 1 ml of ethanol to the 1 ml of incubation mixture. The cells were harvested from each well into individual tubes, the wells were washed with another 1 ml of ethanol, and the washings were combined. The cells were then sonicated and left on ice for 10 minutes. Precipitated proteins were separated by centrifugation, the precipitates were washed once with 1 ml of ethanol, and the supernatants were combined. The final ethanol extract was evaporated under vacuum and the residue dissolved in assay buffer supplied with the cyclic AMP radioimmunoassay kit. Assay for cyclic AMP was carried out using the non-acetylated protocol, precisely as described by the kit manufacturer.

- - -

As described above, thirteen human fetal brain cDNA clones hybridizing under low stringency conditions to a human PCR fragment corresponding to the rat "orphan" receptor, FC5, were isolated from 200,000 screened clones. Eight of these were rescued from the phage vector and were found to share several restriction sites, yet displaying distinct insert sizes. The independent clones hY1-5 and hY1-7 were used for DNA sequencing. Clone hY1-5 had an insert of 2.1 kb that included the entire coding region of the putative homolog of FC5. We found that clone hY1-5 contained 200 bp of 5' untranslated sequence. Preceding the ATG initiation codon at position 197, all three reading frames were interrupted by termination codons. No polyadenylation signal was found at the 3' end of clone hY1-5.

The Nucleotide sequence of the human Y1-receptor cDNA is depicted below:

CCTTCTTTAA TGAAGCAGGA GCGAAAAAGA CAAATTCCAA AGAGGATTGT 50
TCAGTTCAAG GGAATGAAGA ATTCAGAATA ATTTTGGTAA ATGGATTCCA 100
ATATGGGGAA TAAGAATAAG CTGAACAGTT GACCTGCTTT GAAGAAACAT 150

ACTGTCCATT TGTCTAAAAT AATCTATAAC AACCAAACCA ATCAAA 196
ATG AAT TCA ACA TTA TTT TCC CAG GTT GAA AAT CAT TCA 235
GTC CAC TCT AAT TTC TCA GAG AAG AAT GCC CAG CTT CTG 274
GCT TTT GAA AAT GAT GAT TGT CAT CTG CCC TTG GCC ATG 313
ATA TTT ACC TTA GCT CTT GCT TAT GGA GCT GTG ATC ATT 352
CTT GTC TCT GGA AAC CTG GCC TTG ATC ATA ATC ATC TTG 391
AAA CAA AAG GAG ATG AGA AAT GTT ACC AAC ATC CTG ATT 430
GTG AAC CTT TCC TTC TCA GAC TTG CTT GTT GCC ATC ATG 469
TGT CTC CCC TTT ACA TTT GTC TAC ACA TTA ATG GAC CAC 508
TGG GTC TTT GGT GAG GCG ATG TGT AAG TTG AAT CCT TTT 547
GTG CAA TGT GTT TCA ATC ACT GTG TCC ATT TTC TCT CTG 586
GTT CTC ATT GCT GTG GAA CGA CAT CAG CTG ATA ATC AAC 625
CCT CGA GGG TGG AGA CCA AAT AAT AGA CAT GCT TAT GTA 664
GGT ATT GCT GTG ATT TGG GTC CTT GCT GTG GCT TCT TCT 703
TTG CCT TTC CTG ATC TAC CAA GTA ATG ACT GAT GAG CCG 742
TTC CAA AAT GTA ACA CTT GAT GCG TAC AAA GAC AAA TAC 781
GTG TGC TTT GAT CAA TTT CCA TCG GAC TCT CAT AGG TTG 820
TCT TAT ACC ACT CTC CTC TTG GTG CTG CAG TAT TTT GGT 859
CCA CTT TGT TTT ATA TTT ATT TGC TAC TTC AAG ATA TAT 898
ATA CGC CTA AAA AGG AGA AAC AAC ATG ATG GAC AAG ATG 937
AGA GAC AAT AAG TAC AGG TCC AGT GAA ACC AAA AGA ATC 976
AAT ATC ATG CTG CTC TCC ATT GTG GTA GCA TTT GCA GTC 1015
TGC TGG CTC CCT CTT ACC ATC TTT AAC ACT GTG TTT GAT 1054
TGG AAT CAT CAG ATC ATT GCT ACC TGC AAC CAC AAT CTG 1093
TTA TTC CTG CTC TGC CAC CTC ACA GCA ATG ATA TCC ACT 1132
TGT GTC AAC CCC ATA TTT TAT GGG TTC CTG AAC AAA AAC 1171
TTC CAG AGA GAC TTG CAG TTC TTC TTC AAC TTT TGT GAT 1210
TTC CGG TCT CGG GAT GAT GAT TAT GAA ACA ATA GCC ATG 1249
TCC ACG ATG CAC ACA GAT GTT TCC AAA ACT TCT TTG AAG 1288
CAA GCA AGC CCA GTC GCA TTT AAA AAA ATC AAC AAC AAT 1327
GAT GAT AAT GAA AAA ATC TGA AAC TAC TTA TAG CCT ATG 1366
GTC CCG GAT GAC ATC TGT TTA AAA ACA AGC ACA ACC TGC 1405
AAC ATA CTT TGA TTA CCT GTT CTC CCA AGG AAT GGG GTT 1444
GAA ATC ATT TGA AAA TGA CTA AGA TTT TCT TGT CTT GCT 1483

TTT TAC AGT TTT GAC CAG ACA TCT TTG AAG TGC TTT TTG 1522
TGA ATT TAC CAG 1534

Within this sequence, the structural gene for the Y-1 receptor consists of the sequence between nucleotide 197 and 1534. The deduced amino acid sequence of the human Y1-receptor taken from this cDNA sequence is:

Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His
5 10 15
Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
20 25 30
Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu
35 40 45
Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala
50 55 60
Leu Ile Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr
65 70 75
Asn Ile Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala
80 85 90
Ile Met Cys Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His
95 100 105
Trp Val Phe Gly Glu Ala Met Cys Lys Leu Asn Pro Phe Val Gln
110 115 120
Cys Val Ser Ile Thr Val Ser Ile Phe Ser Leu Val Leu Ile Ala
125 130 135
Val Glu Arg His Gln Leu Ile Ile Asn Pro Arg Gly Trp Arg Pro
140 145 150
Asn Asn Arg His Ala Tyr Val Gly Ile Ala Val Ile Trp Val Leu
155 160 165
Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr Gln Val Met Thr
170 175 180
Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr Lys Asp Lys
185 190 195
Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg Leu Ser
200 205 210
Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
215 220 225
Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
230 235 240
Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser
245 250 255
Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val
260 265 270

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Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val
                275                 280                 285
Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu
                290                 295                 300
Leu Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val
                305                 310                 315
Asn Pro Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp
                320                 325                 330
Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp
                335                 340                 345
Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser
                350                 355                 360
Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile
                365                 370                 375
Asn Asn Asn Asp Asp Asn Glu Lys Ile
                380
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The predicted Y1-receptor sequence shows 93% identity to that deduced from the rat FC5 clone, which is proposed to correspond to a rat Y1-receptor. Of the 24 amino acid replacements, seven occur in the N-terminal extracellular part and nine occur in transmembrane region (TM) 4 and the following extracellular loop. The human Y1-sequence has two additional amino acids as compared to its rat counterpart, one in the N-terminal extension and one near the C-terminus. It is notable that the sequence DRY (Asp-Arg-Tyr), which follows TM3 in most receptors belonging to the G-protein-coupled receptor superfamily, reads ERH (Glu-Arg-His) in the Y1 sequences of both human and rat. Most other positions which are highly conserved in the receptor superfamily are also conserved in the predicted Y1-sequences.

The peptides according to the present invention can be synthesized by any suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution addition. Synthetic Y1-receptor according the to the present invention may also be entirely or partially synthesized by recently developed recombinant DNA techniques, which may likely be used for large-scale production.

For example, the techniques of exclusively solid phase synthesis are set forth in "Solid Phase Peptide Synthesis" by Stewart and Young, Freeman & Company, San Francisco (1969), and exemplified in US Patent

4,105,603; fragment condensation methods of synthesis are exemplified in US Patent 3,972,859; and other available synthesis protocols are exemplified in US Patents 3,842,067 and 3,862,925.

Synthesis by use of recombinant DNA techniques, for purposes of the present invention, should be understood to include the suitable employment of a structural gene coding for all or an appropriate section of the Y1-receptor to transform a microorganism, using an expression vector including an appropriate promoter and operator together with the structural gene, and causing the transformed microorganism to express the peptide or such a synthetic peptide fragment. For example, either the complete cDNA sequence for the Y1-receptor peptide depicted above or the structural gene sequence from nucleotide 197 to nucleotide 1534 may be used in recombinant techniques. A non-human animal may also be used to produce the peptide by gene-farming using such a structural gene or cDNA in the microinjection of embryos.

Such recombinant techniques are well known in the field of biotechnology, and can be easily used given the description presented herein.

When the peptides are not prepared using recombinant DNA technology, they are preferably prepared using solid phase synthesis, such as that described by Merrifield [see J. Am. Chem. Soc. 85:2149 (1964), although other equivalent chemical syntheses known in the art can also be used as previously described.

The presence of Y1-receptor mRNA in various human cultured cells was investigated by (1) Northern hybridizations using human Y1-probe (Fig. 1) and (2) by RT-PCR using specific human Y1-primers (data not shown). Both methods showed the human neuroblastoma cell line, SK-N-MC to express Y1-receptors (Fig. 1); this particular cell line has been viewed as a model system for studies on Y1-receptors. The size of the single hybridizing transcript in SK-N-MC is approx. 3.5 kb. By Northern hybridization, we failed to identify Y1-transcripts in several other neuroblastoma cell lines, i.e. IMR (Fig. 1), SH-SY-5Y, LAN1, LAN2, LAN5, 1523 or 2674 (not shown). By using one reverse and three forward primers in RT-PCR, we confirmed the presence of the Y1-

receptor in SK-N-MC, and, in addition, PCR products of the same sizes (350, 520 and 850 bp) were also detected in human cultured circumflex coronary artery smooth muscle cells. The latter observation is in agreement with previous suggestions that the Y1-receptor is expressed in vasculature. The same RT-PCR protocol, which again yielded 350, 520 and 850 bp products when the human fetal brain library was used as template, failed to yield any detectable product in the neuroblastoma cell line, SK-N-BE(2), which is thought to express Y2-receptors. Southern hybridization to human genomic DNA followed by high-stringency washes (Fig.1) suggest that the genome contains a single Y1-receptor gene.

The insert of hY1-5 was transferred to the mammalian expression vector, pCDM8, and used to transfect COS1 cells. Such transfected cells were used for studies on (1) radioligand, i.e. ^{125}I-PYY, binding and (2) second messenger, i.e. Ca^{2+} and cAMP, analyses. As a negative control for all these assays, identical COS1 cells transfected with the rat type-1 angiotensin receptor in the same pCDM8 expression vector were used; in such control cells little or no specific ^{125}I-PYY binding was observed, and no second messenger responses to NPY or PYY.

Radioligand binding assays in membranes prepared from the hY1-5 transfected cells indicate that the clone encodes a protein with the pharmacological characteristics typical of a Y1-receptor type. The dissociation constant (K_d) was 0.86 ± 0.09 nM (n = 4; mean ± SEM), assuming a single-site fit and equal affinity of (porcine) ^{125}I-PYY and unlabeled (porcine) PYY. This kDa is similar to that observed in SK-N-MC and other cell types. The pharmacological profile of ligands competing for ^{125}I-PYY binding to the expressed clone, illustrated in Fig. 2, is also consistent with that of a Y1-receptor. The potency series of PYY ≥ NPY ≥ [Leu^{31}, Pro^{34}]NPY >> NPY2-36 > C2-NPY > (human) PP > NPY13-36 > NPY18-36 was determined (Fig.2); similar rank orders of potency have been observed in various vascular smooth muscle cells [see Br. J. Pharmacol. 105:45 (1992)] and SK-N-MC [see Life Sci. 50 PL7-Pl12 (1992)]. Human NPY was equipotent with porcine NPY (not shown).

Two second messenger responses frequently associated with Y1-receptors are influx of Ca^{2+}, which is not necessarily associated with activation of phosphoinositidase C, and inhibition of cAMP accumulation. Thus, 100 nm of NPY and PYY was found to accelerate in flux of $^{45}Ca^{2+}$, as studied over 2 min, by 135 ± 17% and 157 ± 23% of control, respectively (mean ± SEM; n = 6; two different experiments; $p<0.001$) in hY1-5 transfected COS1 cells; this is similar to the case for endogenous Y1-receptors in SK-N-MC. Control transfected cells did not respond to either NPY or PYY (100 nM). Another well-established characteristic of Y1-receptors, e.g. in SK-N-MC, is the coupling to reduced cAMP accumulation. Likewise, stimulation of the *de novo* expressed Y1-receptor by 100 nM NPY inhibited forskolin (5 µM) elevated accumulation of cAMP in the COS1 cells by 47 ± 55% (mean ± SEM; n = 6; similar results obtained in two different experiments; $p < 0.01$). In the latter experiments, in which the phosphodiesterase inhibitor, methylisobutylxanthine (500 µM) was present throughout, 100 nM NPY also reduced basal cAMP concentrations from 240 ± 14 to 123 ± 4% (pmol of cAMP per 35 mm well; means ± SEM; n = 6; $p < 0.001$).

The heterologously expressed Y1-receptor described herein is thus similar to the endogenous Y1-receptor in brain, and neuroblastoma [5,7] and vascular smooth muscle cells with respect to binding and second messenger properties [see NY Acad. Sci. 611:7 (1990)]. Sequence analysis strongly indicated that the Y1-receptor belongs to the G-protein-coupled receptor superfamily. The human Y1-sequence is, however, only distantly related to the two proposed NPY receptors that have appeared in the literature very recently [see Mol. Pharmacol. 40:869 (1991), and J. Biol. Chem. 267:9 (1992)]. The portion of the sequence spanning the TM regions of hY1-5 shows only 21% and 23% identity with proposed bovine and Drosophila NPY receptors, respectively; the Y1-sequence appears more closely related to tachykinin receptors (29% sequence identity) [see Ann. NY Acad Sci. 632:53 (1991)], and it is similar to the human somatostatin type 1 receptor (23% identity) [see Proc. Natl. Acad. Sci. USA 89:251 (1992)] as to the bovine and Drosophila NPY receptors. Highly divergent sequences

within ligand-receptor families have also been reported for subtypes of amine receptors, however, no other peptide has previously been found to have receptor subtypes which display the degree of sequence divergence that exists between human Y1 (hY1-5) and bovine LCR1 (and Drosophila PR4). For example, the three mammalian tachykinin receptors and the two human somatostatin receptors are 58-67% and 55% identical, respectively, over the regions spanning the TM segments.

In summary, the present invention has described the cloning and identification of the human Y1-type NPY/PYY receptor. This receptor is thought to be instrumental for the ability of NPY/PYY to induce vasoconstriction as well as several behavioral effects.

As stated previously, Neuropeptide Y (NPY) is the most commonly found neurohormonal peptide in the human body. Consequently, the effects of NPY in the organism are many and varied. NPY, like many other messenger molecules, acts by stimulating specific receptor molecules on the cell surface. Previous work has shown that such receptor molecules are heterogenous and that sub-types of receptors thus exist. The receptor sub-type cloned according to the present invention is termed "Y1-receptor", and is widely believed to mediate some of the most important functions of NPY:

(1) Vascular smooth muscle contraction - NPY is released from nerves surrounding blood vessels and is one of the most potent known pressor agents, thus increasing blood pressure in man; elevated levels of NPY have been observed in hypertensive patients;

(2) Sedation/anxiolysis - NPY is as powerful as a benzodiazepine, e.g. Valium, in inducing anticonflict behaviors in animals; in psychiatric patients suffering from major depression, the brain levels of NPY are reduced, and anxiety symptoms in these patients are inversely related to NPY levels; and

(3) Food intake - NPY has frequently been argued to be the most powerful stimulator of food intake and obesity ever studied in mammals; dysregulation of NPY systems have been suggested to exist in patients with eating disorders, i.e. anorexia nervosa/bulimia.

For these and other reasons, the human Y1-receptor according to the present invention has a potential pharmaceutical target; at present, no therapeutically useful drugs are known to interact with the Y1-receptor. Its isolation and cloning according to the present invention should greatly aid in screening efforts and rational drug design aiming to identify novel drugs that may either stimulate, inhibit, or block the Y1-receptor. Such drugs may thus perhaps be useful in the treatment of, e.g., hypertension, depression and/or anxiety, and eating disorders of various kinds as well as obesity. Such screening protocols are well known utilizing other receptors, and these protocols may easily be modified by those skilled in the art to incorporate the use of the Y1-receptor according to the present invention.

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EXAMPLE VI

Production and Testing of Oligonucleotides

The oligonucleotides necessary to study the inhibition of the contractile effect of neuropeptide Y on human blood vessels were synthesized on a Biosearch Cyclone DNA Synthesizer following the manufacturer's instructions. Three oligonucleotides were prepared: (1) an antisense 18-base oligonucleotide (designated as hY1-AS) corresponding to the human Y1 receptor amino-terminus, (2) a corresponding sense oligonucleotide sequence (designated as hY1-S), and (3) a 3-base mismatched antisense oligonucleotide (designated as hY1-MM). The sequences of these three oligonucleotides were:

hY1-S 5' - CAACATTATT TTCCCAGG - 3'

hY1-AS 5' - CCTGGGAAAA TAATGTTG - 3'

hY1-MM 5' - CCTGAGATAA TAAGGTTG - 3'

Following deprotection with 30% ammonium hydroxide using conventional protocols, the oligonucleotides were lyophilized and redissolved in water. These oligonucleotides were then run on a 15% acrylamide gel to verify their sizes.

Subcutaneous arteries and veins from patients operated upon for non-vascular diseases were dissected in the beginning of the operation from the abdominal region and cut into cylindrical segments 2-3 mm

long. These segments were incubated in Dulbecco's Modified Essential Medium (Sigma) supplemented with streptomycin (10,000 mg/ml), penicillin (10,000 U/ml) with or without the test oligonucleotides at 1 μM. Each incubation was conducted for 48 hours at 37° C in humidified 5% carbon dioxide and 95% air.

The cylindrical segments were then mounted on two metal prongs, one of which was connected to a force displacement transducer (model FT03C) attached to a Grass Polygraph for continuous recording of the isometric tension, and the other to a displacement device. The mounted specimens were immersed in temperature controlled (37° C) tissue bathes containing a buffer of the following composition (mM): NaCl 119, $NaHCO_3$ 15, KCl 4.6, MgCl 1.2, NaH_2PO_4 1.2, $CaCl_2$ 1.5, and glucose 11. The solution was continuously gassed with 5% carbon dioxide in oxygen giving a pH of 7.4. A tension of 4 mN was applied to the vessel segments and they were allowed to stabilize at this level of tension for 1.5 hours. The contractile capacity of each vessel segment was examined by exposure to a potassium-rich (60 mM) buffer solution. After another 45 minutes rest period, the following known agonists were added to the vessels in cumulative doses: neuropeptide Y (Auspep, Australia), neuropeptide Y_{13-16} (Bissendorf Biochemicals), pro^{34}neuropeptide, noradrenaline (Sigma).

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In the human subcutaneous arteries and veins examined on day 1 without preincubation, NPY, PYY and Pro34NPY had similar contractile effects while NPY_{13-36} had no contractile effect upon the vessels tested, thus clearly indicating that the contractions seen were mediated by a Y1-receptor.

Despite the 48 hour incubation, the vessels responded with powerful contractions to 60 mM KCl (3.09 ± 0.27 mN), with no difference between the groups receiving or not receiving the oligonucleotides describe above. The contractile responses to neuropeptide Y did not differ between the untreated group (that group receiving no oligonucleotides), the sense oligonucleotide-treated group,

or the vessels incubated with mismatched oligonucleotides either in arteries of veins as depicted in Figure 3 and the following table:

Table 1

Effect of Antisense Oligonucleotide Treatment On Potency and Maximum Contraction in Human Subcutaneous Arteries and Veins

	Maximum Contraction	Potency
Human subcutaneous artery		
Control (no oligonucleotide)	80.8 ± 13.7%	7.49 ± 0.38
Antisense	20.2 ± 6.8%*	7.13 ± 0.15
Sense	79.4 ± 21.7%	7.30 ± 0.19
Mismatch	88.7 ± 39.0	7.24 ± 0.26
Human subcutaneous vein		
Control (no oligonucleotide)	74.3 ± 7.7%	7.61 ± 0.14
Antisense	33.4 ± 5.7%*	7.26 ± 0.24
Sense	57.7 ± 9.3%	7.51 ± 0.21
Mismatch	63.9 ± 28.8%	7.78 ± 0.05

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The maximum contraction (% of potassium-induced contraction) was significantly reduced by antisense oligoncleotide treatment as shown in the above table. In this table, potency is expressed as -log concentration of agonist inducing half maximum concentration, and no significant differences were seen in the potency values between the groups (artery and vein). All values represent the mean ± SEM for 8 to 10 vessel segments, except for the mismatch value which represents 3 segments. The asterisk (*) represents a $p<0.01$ between the sense and antisense data according to the paired Wilcoxon signed rank test.

As seen in Table 1, in both arteries and veins treated with Y1 receptor antisense oligonucleotide the contractile responses to NPY were markedly attenuated. This inhibition did not appear to be competitive in nature, since the potency values were not different between the groups. The responses to noradrenaline (10^{-9} - 10^{-4} M) or 60 mM KCl did not differ between the groups.

As seen, after a 48 hour incubation period with the antisense oligonucleotide (1 μM), the contractile responses to NPY were markedly

reduced. This is believed to be due to reduced numbers of NPY-Y1 receptors. This finding, in turn, indicates that the contractile effect of NPY on human resistance vessels that are likely to be active in the regulation of vascular tone and blood pressure, is mediated primarily by the cloned Y1 receptor. The selectivity of the antisense oligodeoxynucleotide molecule seems to be very high since treatment with the mismatched analogue, hY1-MM, with 3 out of 18 nucleotides mismatched, was without effect on NPY-evoked vasoconstriction. Moreover, the antisense oligonucleotide did not affect responses of the vessels to noradrenaline or high K^+ depolarization.

The antisense oligonucleotides described herein or deemed to be equivalents hereof, may be used in diagnostics, therapeutics and as research reagents and kits. For example, the use of the antisense oligonucleotide compounds may represent a suitable research tool for vascular pharmacology by which the functional characteristics of a number of cloned receptors may be examined. For therapeutic use, the antisense oligonucleotides according to the present invention is to be administered to an animal, especially a human, in which it is medically desired to specifically attenuate NPY-evoked vasoconstriction. Administration of the antisense oligonucleotides according to the present invention may be by any acceptable means, however, it is most preferred that the administration take place intravenously into a blood vessel, either artery or vein, so as to deliver the oligonucleotide directly to the site of NPY receptors. Use of recognized pharmacologically acceptable carriers may also be preferred as carriers, diluents, buffers and other functional classes well within the purview of those skilled in the formulation arts. The exact dosages of antisense oligonucleotides provided to a mammal to attenuate the NPY-evoked response in the mammal's blood vessels may vary across a broad range, however, such dosages should be limited to that range which is sufficient to bring about the desired degree of attenuation based upon the method of administration, the urgency by which such attenuation is desired, the weight of the mammal, and the amount of the oligonucleotide in the total bolus of medication administered. Such

variables are well within the purview of those skilled in the compounding and administration arts, and thus uniqueness for the use of antisense oligonucleotides to the human NPY receptor is not to be predicated upon any specific amount of oligonucleotide being administered to the mammal in which vasoconstriction inhibition is desired.

A list of the nucleic acid and amino acid sequences which comprise the present invention follows:

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Claes R. Wahlestedt

(iii) NUMBER OF SEQUENCES: 6

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CCTTCTTTAA TGAAGCAGGA GCGAAAAAGA CAAATTCCAA AGAGGATTGT   50
TCAGTTCAAG GGAATGAAGA ATTCAGAATA ATTTTGGTAA ATGGATTCCA  100
ATATGGGGAA TAAGAATAAG CTGAACAGTT GACCTGCTTT GAAGAAACAT  150
ACTGTCCATT TGTCTAAAAT AATCTATAAC AACCAAACCA ATCAAA       196
ATG AAT TCA ACA TTA TTT TCC CAG GTT GAA AAT CAT TCA  235
GTC CAC TCT AAT TTC TCA GAG AAG AAT GCC CAG CTT CTG  274
GCT TTT GAA AAT GAT GAT TGT CAT CTG CCC TTG GCC ATG  313
ATA TTT ACC TTA GCT CTT GCT TAT GGA GCT GTG ATC ATT  352
CTT GTC TCT GGA AAC CTG GCC TTG ATC ATA ATC ATC TTG  391
AAA CAA AAG GAG ATG AGA AAT GTT ACC AAC ATC CTG ATT  430
GTG AAC CTT TCC TTC TCA GAC TTG CTT GTT GCC ATC ATG  469
TGT CTC CCC TTT ACA TTT GTC TAC ACA TTA ATG GAC CAC  508
TGG GTC TTT GGT GAG GCG ATG TGT AAG TTG AAT CCT TTT  547
GTG CAA TGT GTT TCA ATC ACT GTG TCC ATT TTC TCT CTG  586
GTT CTC ATT GCT GTG GAA CGA CAT CAG CTG ATA ATC AAC  625
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CCT CGA GGG TGG AGA CCA AAT AAT AGA CAT GCT TAT GTA 664
GGT ATT GCT GTG ATT TGG GTC CTT GCT GTG GCT TCT TCT 703
TTG CCT TTC CTG ATC TAC CAA GTA ATG ACT GAT GAG CCG 742
TTC CAA AAT GTA ACA CTT GAT GCG TAC AAA GAC AAA TAC 781
GTG TGC TTT GAT CAA TTT CCA TCG GAC TCT CAT AGG TTG 820
TCT TAT ACC ACT CTC CTC TTG GTG CTG CAG TAT TTT GGT 859
CCA CTT TGT TTT ATA TTT ATT TGC TAC TTC AAG ATA TAT 898
ATA CGC CTA AAA AGG AGA AAC AAC ATG ATG GAC AAG ATG 937
AGA GAC AAT AAG TAC AGG TCC AGT GAA ACC AAA AGA ATC 976
AAT ATC ATG CTG CTC TCC ATT GTG GTA GCA TTT GCA GTC 1015
TGC TGG CTC CCT CTT ACC ATC TTT AAC ACT GTG TTT GAT 1054
TGG AAT CAT CAG ATC ATT GCT ACC TGC AAC CAC AAT CTG 1093
TTA TTC CTG CTC TGC CAC CTC ACA GCA ATG ATA TCC ACT 1132
TGT GTC AAC CCC ATA TTT TAT GGG TTC CTG AAC AAA AAC 1171
TTC CAG AGA GAC TTG CAG TTC TTC TTC AAC TTT TGT GAT 1210
TTC CGG TCT CGG GAT GAT GAT TAT GAA ACA ATA GCC ATG 1249
TCC ACG ATG CAC ACA GAT GTT TCC AAA ACT TCT TTG AAG 1288
CAA GCA AGC CCA GTC GCA TTT AAA AAA ATC AAC AAC AAT 1327
GAT GAT AAT GAA AAA ATC TGA AAC TAC TTA TAG CCT ATG 1366
GTC CCG GAT GAC ATC TGT TTA AAA ACA AGC ACA ACC TGC 1405
AAC ATA CTT TGA TTA CCT GTT CTC CCA AGG AAT GGG GTT 1444
GAA ATC ATT TGA AAA TGA CTA AGA TTT TCT TGT CTT GCT 1483
TTT TAC AGT TTT GAC CAG ACA TCT TTG AAG TGC TTT TTG 1522
TGA ATT TAC CAG 1534

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAT TCA ACA TTA TTT TCC CAG GTT GAA AAT CAT TCA 39
GTC CAC TCT AAT TTC TCA GAG AAG AAT GCC CAG CTT CTG 78
GCT TTT GAA AAT GAT GAT TGT CAT CTG CCC TTG GCC ATG 117

ATA TTT ACC TTA GCT CTT GCT TAT GGA GCT GTG ATC ATT 156
CTT GTC TCT GGA AAC CTG GCC TTG ATC ATA ATC ATC TTG 195
AAA CAA AAG GAG ATG AGA AAT GTT ACC AAC ATC CTG ATT 234
GTG AAC CTT TCC TTC TCA GAC TTG CTT GTT GCC ATC ATG 273
TGT CTC CCC TTT ACA TTT GTC TAC ACA TTA ATG GAC CAC 312
TGG GTC TTT GGT GAG GCG ATG TGT AAG TTG AAT CCT TTT 351
GTG CAA TGT GTT TCA ATC ACT GTG TCC ATT TTC TCT CTG 390
GTT CTC ATT GCT GTG GAA CGA CAT CAG CTG ATA ATC AAC 429
CCT CGA GGG TGG AGA CCA AAT AAT AGA CAT GCT TAT GTA 468
GGT ATT GCT GTG ATT TGG GTC CTT GCT GTG GCT TCT TCT 507
TTG CCT TTC CTG ATC TAC CAA GTA ATG ACT GAT GAG CCG 546
TTC CAA AAT GTA ACA CTT GAT GCG TAC AAA GAC AAA TAC 585
GTG TGC TTT GAT CAA TTT CCA TCG GAC TCT CAT AGG TTG 624
TCT TAT ACC ACT CTC CTC TTG GTG CTG CAG TAT TTT GGT 663
CCA CTT TGT TTT ATA TTT ATT TGC TAC TTC AAG ATA TAT 702
ATA CGC CTA AAA AGG AGA AAC AAC ATG ATG GAC AAG ATG 741
AGA GAC AAT AAG TAC AGG TCC AGT GAA ACC AAA AGA ATC 780
AAT ATC ATG CTG CTC TCC ATT GTG GTA GCA TTT GCA GTC 819
TGC TGG CTC CCT CTT ACC ATC TTT AAC ACT GTG TTT GAT 858
TGG AAT CAT CAG ATC ATT GCT ACC TGC AAC CAC AAT CTG 897
TTA TTC CTG CTC TGC CAC CTC ACA GCA ATG ATA TCC ACT 936
TGT GTC AAC CCC ATA TTT TAT GGG TTC CTG AAC AAA AAC 975
TTC CAG AGA GAC TTG CAG TTC TTC TTC AAC TTT TGT GAT 1014
TTC CGG TCT CGG GAT GAT GAT TAT GAA ACA ATA GCC ATG 1053
TCC ACG ATG CAC ACA GAT GTT TCC AAA ACT TCT TTG AAG 1092
CAA GCA AGC CCA GTC GCA TTT AAA AAA ATC AAC AAC AAT 1131
GAT GAT AAT GAA AAA ATC TGA AAC TAC TTA TAG CCT ATG 1170
GTC CCG GAT GAC ATC TGT TTA AAA ACA AGC ACA ACC TGC 1209
AAC ATA CTT TGA TTA CCT GTT CTC CCA AGG AAT GGG GTT 1248
GAA ATC ATT TGA AAA TGA CTA AGA TTT TCT TGT CTT GCT 1287
TTT TAC AGT TTT GAC CAG ACA TCT TTG AAG TGC TTT TTG 1326
TGA ATT TAC CAG 1338

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His
 5                  10                  15
Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
            20                  25                  30
Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu
        35                  40                  45
Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala
    50                  55                  60
Leu Ile Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr
65                  70                  75
Asn Ile Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala
                80                  85                  90
Ile Met Cys Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His
            95                  100                 105
Trp Val Phe Gly Glu Ala Met Cys Lys Leu Asn Pro Phe Val Gln
        110                 115                 120
Cys Val Ser Ile Thr Val Ser Ile Phe Ser Leu Val Leu Ile Ala
    125                 130                 135
Val Glu Arg His Gln Leu Ile Ile Asn Pro Arg Gly Trp Arg Pro
140                 145                 150
Asn Asn Arg His Ala Tyr Val Gly Ile Ala Val Ile Trp Val Leu
155                 160                 165
Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr Gln Val Met Thr
            170                 175                 180
Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr Lys Asp Lys
        185                 190                 195
Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg Leu Ser
    200                 205                 210
Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
215                 220                 225
Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
            230                 235                 240
Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser
        245                 250                 255
Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val
    260                 265                 270
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Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val
275 280 285
Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu
290 295 300
Leu Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val
305 310 315
Asn Pro Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp
320 325 330
Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp
335 340 345
Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser
350 355 360
Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile
365 370 375
Asn Asn Asn Asp Asp Asn Glu Lys Ile
380

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAACATTATT TTCCCAGG 18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCTGGGAAAA TAATGTTG 18

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCTGAGATAA TAAGGTTG 18

Thus while I have illustrated and described the preferred embodiment of my invention, it is to be understood that this invention is capable of variation and modification, and I therefore do not wish to be limited to the precise terms set forth, but desire to avail myself of such changes and alterations which may be made for adapting the invention to various usages and conditions. Such variations and modifications, for example, would include the substitution of structurally similar nucleic and amino acid sequences which function to yield substantially similar activities to those specifically described above. Thus, changes in sequence by the substitution, deletion, insertion or addition of nucleic acids (in the DNA sequences), or substitution of completely different antisense sequences which do not substantially alter the function of those sequences specifically described above, are deemed to be within the scope of the present invention. Accordingly, such changes and alterations are properly intended to be within the full range of equivalents, and therefore within the purview of the following claims.

Having thus described my invention and the manner and a process of making and using it in such full, clear, concise and exact terms so as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same;

I claim:

1. An antisense oligonucleotide sequence, corresponding to the amino-terminus of the human Y1 receptor, that is 5' - CCTGGGAAAA TAATGTTG - 3', said sequence being further characterized as having the specific pharmacologic action of attenuating neuropeptide Y-evoked vasoconstriction in human arteries and veins.

2. A method for attenuating neuropeptide Y-evoked contractile response in a mammalien blood vessel which comprises contacting human Y1 receptors affecting the contractile response with an antisense oligonucleotide to the receptor in an amount sufficient to bring about an attenuation of the neuropeptide Y-evoked response.

3. A method according to Claim 2 in which the antisense oligonucleotide is 5' - CCTGGGAAAA TAATGTTG - 3'.

4. A cDNA for the genetic encoding of the human neuropeptide Y/peptide YY Y-1 receptor which is

CCTTCTTTAA TGAAGCAGGA GCGAAAAAGA CAAATTCCAA AGAGGATTGT 50
TCAGTTCAAG GGAATGAAGA ATTCAGAATA ATTTTGGTAA ATGGATTCCA 100
ATATGGGGAA TAAGAATAAG CTGAACAGTT GACCTGCTTT GAAGAAACAT 150
ACTGTCCATT TGTCTAAAAT AATCTATAAC AACCAAACCA ATCAAA 196
ATG AAT TCA ACA TTA TTT TCC CAG GTT GAA AAT CAT TCA 235
GTC CAC TCT AAT TTC TCA GAG AAG AAT GCC CAG CTT CTG 274
GCT TTT GAA AAT GAT GAT TGT CAT CTG CCC TTG GCC ATG 313
ATA TTT ACC TTA GCT CTT GCT TAT GGA GCT GTG ATC ATT 352
CTT GTC TCT GGA AAC CTG GCC TTG ATC ATA ATC ATC TTG 391
AAA CAA AAG GAG ATG AGA AAT GTT ACC AAC ATC CTG ATT 430
GTG AAC CTT TCC TTC TCA GAC TTG CTT GTT GCC ATC ATG 469
TGT CTC CCC TTT ACA TTT GTC TAC ACA TTA ATG GAC CAC 508
TGG GTC TTT GGT GAG GCG ATG TGT AAG TTG AAT CCT TTT 547
GTG CAA TGT GTT TCA ATC ACT GTG TCC ATT TTC TCT CTG 586
GTT CTC ATT GCT GTG GAA CGA CAT CAG CTG ATA ATC AAC 625
CCT CGA GGG TGG AGA CCA AAT AAT AGA CAT GCT TAT GTA 664
GGT ATT GCT GTG ATT TGG GTC CTT GCT GTG GCT TCT TCT 703
TTG CCT TTC CTG ATC TAC CAA GTA ATG ACT GAT GAG CCG 742
TTC CAA AAT GTA ACA CTT GAT GCG TAC AAA GAC AAA TAC 781

GTG TGC TTT GAT CAA TTT CCA TCG GAC TCT CAT AGG TTG 820
TCT TAT ACC ACT CTC CTC TTG GTG CTG CAG TAT TTT GGT 859
CCA CTT TGT TTT ATA TTT ATT TGC TAC TTC AAG ATA TAT 898
ATA CGC CTA AAA AGG AGA AAC AAC ATG ATG GAC AAG ATG 937
AGA GAC AAT AAG TAC AGG TCC AGT GAA ACC AAA AGA ATC 976
AAT ATC ATG CTG CTC TCC ATT GTG GTA GCA TTT GCA GTC 1015
TGC TGG CTC CCT CTT ACC ATC TTT AAC ACT GTG TTT GAT 1054
TGG AAT CAT CAG ATC ATT GCT ACC TGC AAC CAC AAT CTG 1093
TTA TTC CTG CTC TGC CAC CTC ACA GCA ATG ATA TCC ACT 1132
TGT GTC AAC CCC ATA TTT TAT GGG TTC CTG AAC AAA AAC 1171
TTC CAG AGA GAC TTG CAG TTC TTC TTC AAC TTT TGT GAT 1210
TTC CGG TCT CGG GAT GAT GAT TAT GAA ACA ATA GCC ATG 1249
TCC ACG ATG CAC ACA GAT GTT TCC AAA ACT TCT TTG AAG 1288
CAA GCA AGC CCA GTC GCA TTT AAA AAA ATC AAC AAC AAT 1327
GAT GAT AAT GAA AAA ATC TGA AAC TAC TTA TAG CCT ATG 1366
GTC CCG GAT GAC ATC TGT TTA AAA ACA AGC ACA ACC TGC 1405
AAC ATA CTT TGA TTA CCT GTT CTC CCA AGG AAT GGG GTT 1444
GAA ATC ATT TGA AAA TGA CTA AGA TTT TCT TGT CTT GCT 1483
TTT TAC AGT TTT GAC CAG ACA TCT TTG AAG TGC TTT TTG 1522
TGA ATT TAC CAG 1534.

5. A cDNA according to Claim 4 which is the structural gene for human neuropeptide Y/peptide YY Y-1 receptor and which is:

ATG AAT TCA ACA TTA TTT TCC CAG GTT GAA AAT CAT TCA 39
GTC CAC TCT AAT TTC TCA GAG AAG AAT GCC CAG CTT CTG 78
GCT TTT GAA AAT GAT GAT TGT CAT CTG CCC TTG GCC ATG 117
ATA TTT ACC TTA GCT CTT GCT TAT GGA GCT GTG ATC ATT 156
CTT GTC TCT GGA AAC CTG GCC TTG ATC ATA ATC ATC TTG 195
AAA CAA AAG GAG ATG AGA AAT GTT ACC AAC ATC CTG ATT 234
GTG AAC CTT TCC TTC TCA GAC TTG CTT GTT GCC ATC ATG 273
TGT CTC CCC TTT ACA TTT GTC TAC ACA TTA ATG GAC CAC 312
TGG GTC TTT GGT GAG GCG ATG TGT AAG TTG AAT CCT TTT 351
GTG CAA TGT GTT TCA ATC ACT GTG TCC ATT TTC TCT CTG 390
GTT CTC ATT GCT GTG GAA CGA CAT CAG CTG ATA ATC AAC 429
CCT CGA GGG TGG AGA CCA AAT AAT AGA CAT GCT TAT GTA 468

GGT ATT GCT GTG ATT TGG GTC CTT GCT GTG GCT TCT TCT 507
TTG CCT TTC CTG ATC TAC CAA GTA ATG ACT GAT GAG CCG 546
TTC CAA AAT GTA ACA CTT GAT GCG TAC AAA GAC AAA TAC 585
GTG TGC TTT GAT CAA TTT CCA TCG GAC TCT CAT AGG TTG 624
TCT TAT ACC ACT CTC CTC TTG GTG CTG CAG TAT TTT GGT 663
CCA CTT TGT TTT ATA TTT ATT TGC TAC TTC AAG ATA TAT 702
ATA CGC CTA AAA AGG AGA AAC AAC ATG ATG GAC AAG ATG 741
AGA GAC AAT AAG TAC AGG TCC AGT GAA ACC AAA AGA ATC 780
AAT ATC ATG CTG CTC TCC ATT GTG GTA GCA TTT GCA GTC 819
TGC TGG CTC CCT CTT ACC ATC TTT AAC ACT GTG TTT GAT 858
TGG AAT CAT CAG ATC ATT GCT ACC TGC AAC CAC AAT CTG 897
TTA TTC CTG CTC TGC CAC CTC ACA GCA ATG ATA TCC ACT 936
TGT GTC AAC CCC ATA TTT TAT GGG TTC CTG AAC AAA AAC 975
TTC CAG AGA GAC TTG CAG TTC TTC TTC AAC TTT TGT GAT 1014
TTC CGG TCT CGG GAT GAT GAT TAT GAA ACA ATA GCC ATG 1053
TCC ACG ATG CAC ACA GAT GTT TCC AAA ACT TCT TTG AAG 1092
CAA GCA AGC CCA GTC GCA TTT AAA AAA ATC AAC AAC AAT 1131
GAT GAT AAT GAA AAA ATC TGA AAC TAC TTA TAG CCT ATG 1170
GTC CCG GAT GAC ATC TGT TTA AAA ACA AGC ACA ACC TGC 1209
AAC ATA CTT TGA TTA CCT GTT CTC CCA AGG AAT GGG GTT 1248
GAA ATC ATT TGA AAA TGA CTA AGA TTT TCT TGT CTT GCT 1287
TTT TAC AGT TTT GAC CAG ACA TCT TTG AAG TGC TTT TTG 1326
TGA ATT TAC CAG 1338

6. The isolated peptide

Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His
5 10 15
Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
20 25 30
Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu
35 40 45
Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala
50 55 60
Leu Ile Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr
65 70 75
Asn Ile Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala
80 85 90

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Ile Met Cys Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His
                 95                  100                 105
Trp Val Phe Gly Glu Ala Met Cys Lys Leu Asn Pro Phe Val Gln
                110                 115                 120
Cys Val Ser Ile Thr Val Ser Ile Phe Ser Leu Val Leu Ile Ala
                125                 130                 135
Val Glu Arg His Gln Leu Ile Ile Asn Pro Arg Gly Trp Arg Pro
                140                 145                 150
Asn Asn Arg His Ala Tyr Val Gly Ile Ala Val Ile Trp Val Leu
                155                 160                 165
Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr Gln Val Met Thr
                170                 175                 180
Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr Lys Asp Lys
                185                 190                 195
Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg Leu Ser
                200                 205                 210
Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
                215                 220                 225
Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
                230                 235                 240
Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser
                245                 250                 255
Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val
                260                 265                 270
Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val
                275                 280                 285
Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu
                290                 295                 300
Leu Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val
                305                 310                 315
Asn Pro Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp
                320                 325                 330
Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp
                335                 340                 345
Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser
                350                 355                 360
Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile
                365                 370                 375
Asn Asn Asn Asp Asp Asn Glu Lys Ile
            380
```

7. A method for screening compounds for the treatment of a condition brought about by other than normal clinical amounts of neuropeptide Y in a patient which comprises bringing said compound in

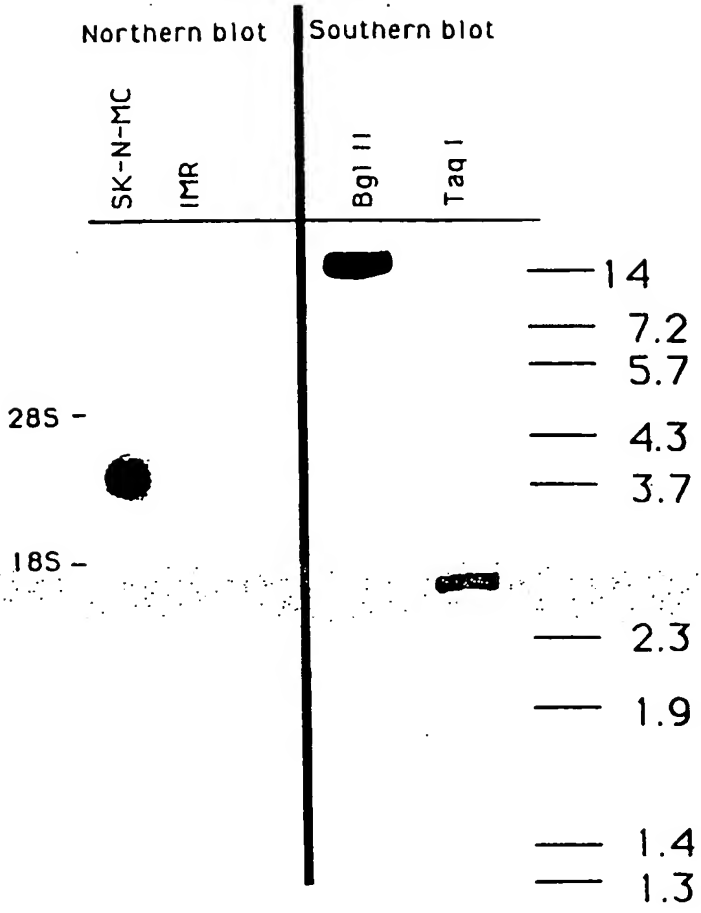
contact with an isolated human Y1-receptor peptide, or a fragment thereof having Neuropeptide Y activity, having the amino acid sequence:

```
Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His
                5                  10                  15
Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
            20                  25                  30
Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu
        35                  40                  45
Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala
    50                  55                  60
Leu Ile Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr
65                  70                  75
Asn Ile Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala
            80                  85                  90
Ile Met Cys Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His
        95                  100                 105
Trp Val Phe Gly Glu Ala Met Cys Lys Leu Asn Pro Phe Val Gln
    110                 115                 120
Cys Val Ser Ile Thr Val Ser Ile Phe Ser Leu Val Leu Ile Ala
125                 130                 135
Val Glu Arg His Gln Leu Ile Ile Asn Pro Arg Gly Trp Arg Pro
            140                 145                 150
Asn Asn Arg His Ala Tyr Val Gly Ile Ala Val Ile Trp Val Leu
        155                 160                 165
Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr Gln Val Met Thr
    170                 175                 180
Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr Lys Asp Lys
185                 190                 195
Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg Leu Ser
            200                 205                 210
Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
        215                 220                 225
Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
    230                 235                 240
Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser
245                 250                 255
Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val
            260                 265                 270
Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val
        275                 280                 285
Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu
    290                 295                 300
```

```
Leu Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val
                305                 310                 315
Asn Pro Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp
                320                 325                 330
Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp
                335                 340                 345
Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser
                350                 355                 360
Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile
                365                 370                 375
Asn Asn Asn Asp Asp Asn Glu Lys Ile
                380
```

and determining whether said compound stimulates, inhibits or blocks the human Y1-receptor following conventional screening protocols.

FIGURE 1


Northern blot
Southern blot
SK-N-MC
IMR
Bgl II
Taq I
14
7.2
5.7
4.3
3.7
2.3
1.9
1.4
1.3
28S
18S

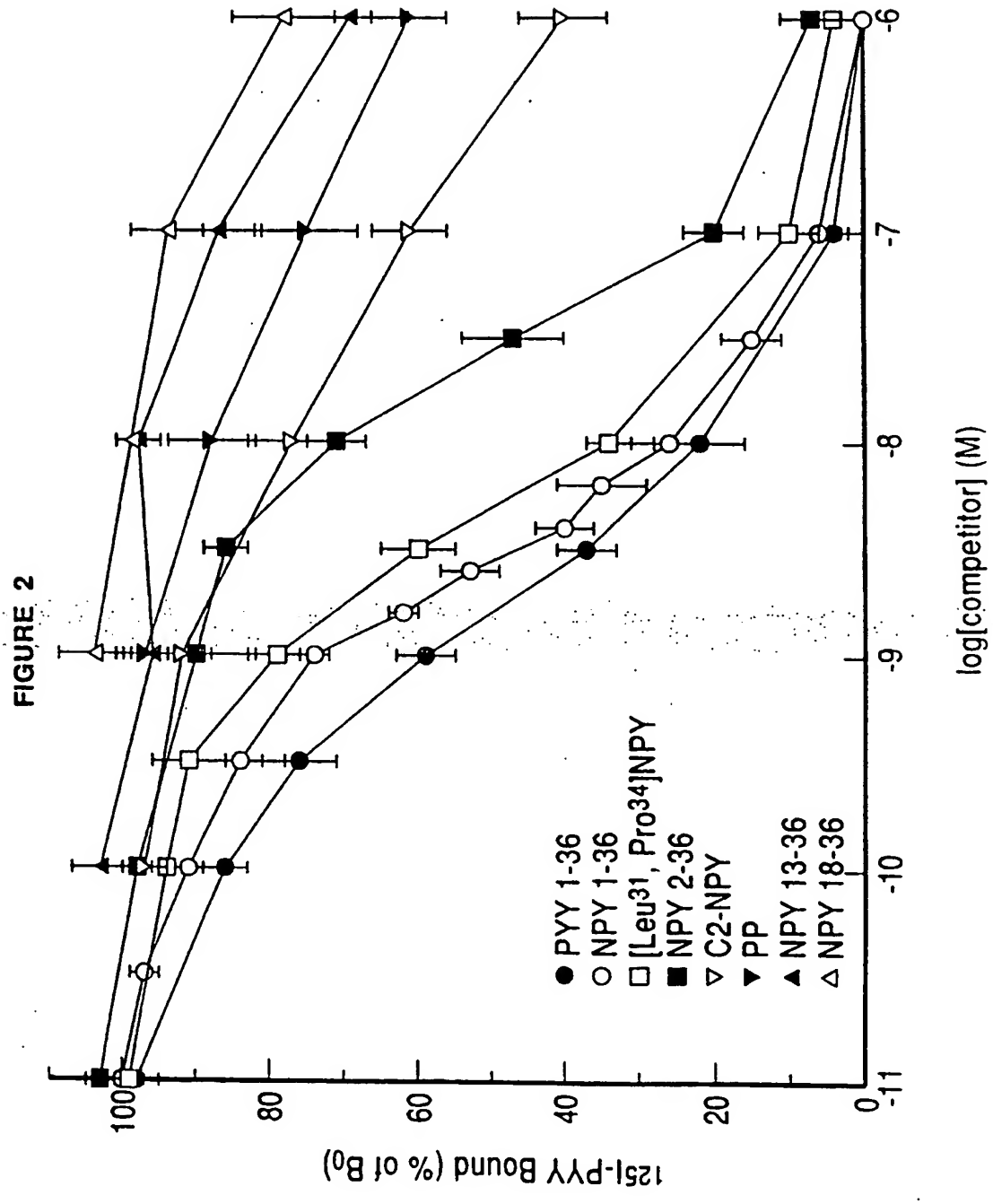

125I-PYY Bound (% of B0)
100
80
60
40
20
0
-11
-10
-9
-8
-7
-6
log[competitor] (M)
● PYY 1-36
○ NPY 1-36
□ [Leu31, Pro34]NPY
■ NPY 2-36
▽ C2-NPY
▼ PP
▲ NPY 13-36
△ NPY 18-36

FIGURE 2

FIGURE 3

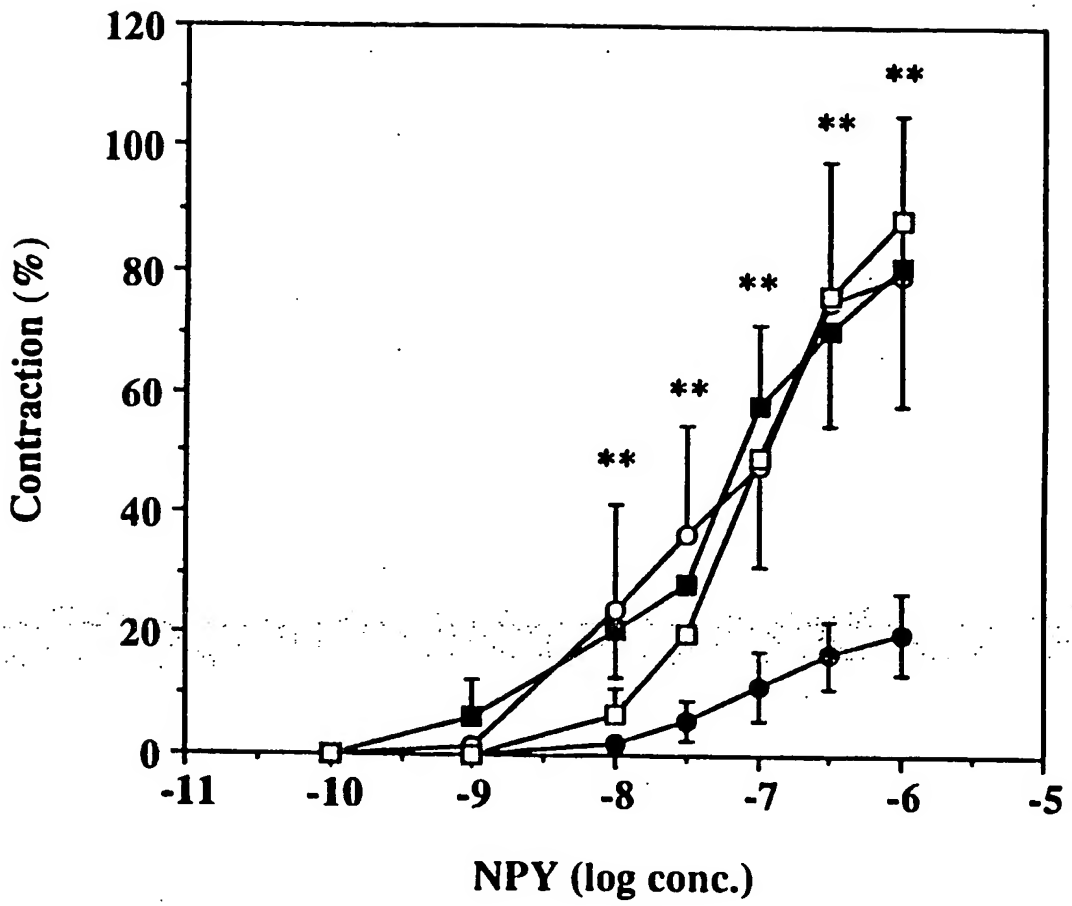
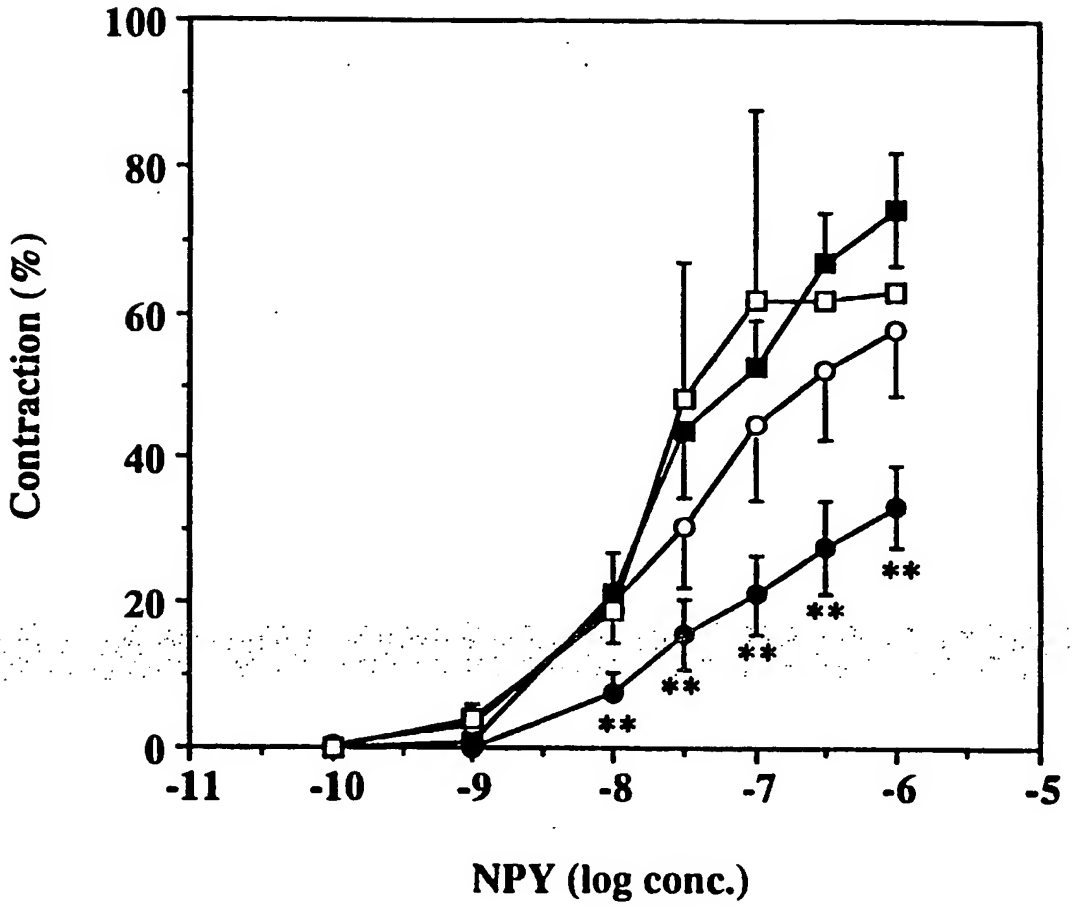


FIGURE 4



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/05039

A. CLASSIFICATION OF SUBJECT MATTER
IPC(5) :C07H 21/04; C12N 1/21, 5/00; C12P 21/00
US CL :536/23.1; 530/350; 514/12/ 435/6
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 530/350; 514/12; 435/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, Medline, Dialog
search terms: neuropeptide Y, peptide YY, receptor

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	The Journal of Biological Chemistry, Volume 267, No. 1, issued 05 January 1992, X. Li et al, "Cloning, Functional Expression, and Developmental Regulation of a Neuropeptide Y Receptor from Drosophila Melanogaster", pages 9-12, see abstract.	1-8
Y	European Journal of Pharmacology, Volume 204, issued 1991, H. N. Doods et al, "Different Neuropeptide Y Receptor Subtypes in Rat and Rabbit Vas Deferens", pages 101-103, see abstract.	1-8

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be part of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search
20 AUGUST 1993

Date of mailing of the international search report
SEP 13 1993

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/05039

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Molecular Pharmacolog, Volume 40, issued 1991, J. Rimland et al, "Sequence and Expression of a Neuropeptide Y Receptor cDNA", pages 869-875, see abstract.	1-8
Y	Annals of the New York Academy of Sciences, Volume 611, issued 01 December 1990, C. Wahlestedt et al, "Central and Peripheral Significance of Neuropeptide Y and its Related Peptides", pages 7-26, see pages 11-18.	1-8